

BEST AVAILABLE COPY

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/007,078

ENTERED

CRF Processing Date: 12/11/2001

Edited by: Ar

Verified by: Ar

OIPE

TECH CENTER 1600/2900

FEB 06 2002

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- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: globally deleted duplicate <2207's

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

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FEB 06 2002
TECH CENTER 160012900

1614

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/007,078

DATE: 12/31/2001

TIME: 18:46:52

Input Set : A:\pto.amc.txt

Output Set: N:\CRF3\12312001\J007078.raw

P.S

#2

4 <110> APPLICANT: Donna T. Ward
5 Andrew T. Watt
7 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF EIF2C1 EXPRESSION
9 <130> FILE REFERENCE: RTS-0236
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/007,078
C--> 11 <141> CURRENT FILING DATE: 2001-11-08
11 <160> NUMBER OF SEQ ID NOS: 88
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 20
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial Sequence
19 <220> FEATURE:
21 <223> OTHER INFORMATION: Antisense Oligonucleotide
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29 <212> TYPE: DNA
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41 <211> LENGTH: 7478
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43 <213> ORGANISM: Homo sapiens
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47 <221> NAME/KEY: CDS
48 <222> LOCATION: (214)...(2787)
50 <400> SEQUENCE: 3
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53 gggatcccga gcagcgagag tgtggggtac ctaggcccct cacgctggac ttacagtct 180
54 ccggggccgcc tgacctccgc acgggtatat ggg atg gaa gcg gga ccc tcg gga 234
55 Met Glu Ala Gly Pro Ser Gly
56 1 5
58 gca gct gcg ggc gct tac ctg ccc ccc ctg cag cag gtg ttc cag gca 282
59 Ala Ala Ala Gly Ala Tyr Leu Pro Leu Gln Gln Val Phe Gln Ala
60 10 15 20
62 cct cgc cgg cct ggc att ggc act gtg ggg aaa cca atc aag ctc ctg 330
63 Pro Arg Arg Pro Gly Ile Gly Thr Val Gly Lys Pro Ile Lys Leu Leu
64 25 30 35
66 gcc aat tac ttt gag gtg gac atc cct aag atc gac gtg tac cac tac 378
67 Ala Asn Tyr Phe Glu Val Asp Ile Pro Lys Ile Asp Val Tyr His Tyr
68 40 45 50 55
70 gag gtg gac atc aag ccg gat aag tgt ccc cgt aga gtc aac cgg gaa 426

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74 gtg gtg gaa tac atg gtc cag cat ttc aag cct cag atc ttt ggt gat      474
75 Val Val Glu Tyr Met Val Gln His Phe Lys Pro Gln Ile Phe Gly Asp
76          75          80          85
78 cgc aag cct gtg tat gat gga aag aag aac att tac act gtc aca gca      522
79 Arg Lys Pro Val Tyr Asp Gly Lys Lys Asn Ile Tyr Thr Val Thr Ala
80          90          95          100
82 ctg ccc att ggc aac gaa cgg gtc gac ttt gag gtg aca atc cct ggg      570
83 Leu Pro Ile Gly Asn Glu Arg Val Asp Phe Glu Val Thr Ile Pro Gly
84          105          110          115
86 gaa ggg aag gat cga atc ttt aag gtc tcc atc aag tgg cta gcc att      618
87 Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Leu Ala Ile
88 120          125          130          135
90 gtg agc tgg cga atg ctg cat gag gcc ctg gtc agc ggc cag atc cct      666
91 Val Ser Trp Arg Met Leu His Glu Ala Leu Val Ser Gly Gln Ile Pro
92          140          145          150
94 gtt ccc ttg gag tct gtg caa gcc ctg gat gtg gcc atg agg cac ctg      714
95 Val Pro Leu Glu Ser Val Gln Ala Leu Asp Val Ala Met Arg His Leu
96          155          160          165
98 gca tcc atg agg tac acc cct gtg ggc cgc tcc ttc ttc tca cgc cct      762
99 Ala Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Ser Pro Pro
100          170          175          180
102 gag ggc tac tac cac ccg ctg ggg ggt ggg cgc gaa gtc tgg ttc ggc      810
103 Glu Gly Tyr Tyr His Pro Leu Gly Gly Gly Arg Glu Val Trp Phe Gly
104          185          190          195
106 ttt cac cag tct gtg cgc cct gcc atg tgg aag atg atg ctc aac att      858
107 Phe His Gln Ser Val Arg Pro Ala Met Trp Lys Met Met Leu Asn Ile
108 200          205          210          215
110 gat gtc tca gcc act gcc ttt tat aag gca cag cca gtg att gag ttc      906
111 Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu Phe
112          220          225          230
114 atg tgt gag gtg ctg gac atc agg aac ata gat gag cag ccc aag ccc      954
115 Met Cys Glu Val Leu Asp Ile Arg Asn Ile Asp Glu Gln Pro Lys Pro
116          235          240          245
118 ctc acg gac tct cag cgc gtt cgc ttc acc aag gag atc aag ggc ctg      1002
119 Leu Thr Asp Ser Gln Arg Val Arg Phe Thr Lys Glu Ile Lys Gly Leu
120          250          255          260
122 aag gtg gaa gtc acc cac tgt gga cag atg aag agg aag tac cgc gtg      1050
123 Lys Val Glu Val Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg Val
124          265          270          275
126 tgt aat gtt acc cgt cgc cct gct agc cat cag aca ttc ccc tta cag      1098
127 Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu Gln
128 280          285          290          295
130 ctg gag agt gga cag act gtg gag tgc aca gtg gca cag tat ttc aag      1146
131 Leu Glu Ser Gly Gln Thr Val Glu Cys Thr Val Ala Gln Tyr Phe Lys
132          300          305          310
134 cag aaa tat aac ctt cag ctc aag tat ccc cat ctg ccc tgc cta caa      1194
135 Gln Lys Tyr Asn Leu Gln Leu Lys Tyr Pro His Leu Pro Cys Leu Gln

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136		315		320		325		
138	gtt ggc cag gaa caa aag cat acc tac ctt ccc cta gag gtc tgt aac							1242
139	Val Gly Gln Glu Gln Lys His Thr Tyr Leu Pro Leu Glu Val Cys Asn							
140		330		335		340		
142	att gtg gct ggg cag cgc tgt att aag aag ctg acc gac aac cag acc							1290
143	Ile Val Ala Gly Gln Arg Cys Ile Lys Lys Leu Thr Asp Asn Gln Thr							
144		345		350		355		
146	tcg acc atg ata aag gcc aca gct aga tcc gct cca gac aga cag gag							1338
147	Ser Thr Met Ile Lys Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln Glu							
148	360		365		370		375	
150	gag atc agt cgc ctg atg aag aat gcc agc tac aac tta gat ccc tac							1386
151	Glu Ile Ser Arg Leu Met Lys Asn Ala Ser Tyr Asn Leu Asp Pro Tyr							
152		380		385		390		
154	atc cag gaa ttt ggg atc aaa gtg aag gat gac atg acg gag gtg aca							1434
155	Ile Gln Glu Phe Gly Ile Lys Val Lys Asp Asp Met Thr Glu Val Thr							
156		395		400		405		
158	ggg cga gtg ctg ccg gcg ccc atc ttg cag tac ggc ggc cgg aac cgg							1482
159	Gly Arg Val Leu Pro Ala Pro Ile Leu Gln Tyr Gly Gly Arg Asn Arg							
160		410		415		420		
162	gcc att gcc aca ccc aat cag ggt gtc tgg gac atg cgg ggg aaa cag							1530
163	Ala Ile Ala Thr Pro Asn Gln Gly Val Trp Asp Met Arg Gly Lys Gln							
164		425		430		435		
166	ttc tac aat ggg att gag atc aaa gtc tgg gcc atc gcc tgc ttc gca							1578
167	Phe Tyr Asn Gly Ile Glu Ile Lys Val Trp Ala Ile Ala Cys Phe Ala							
168	440		445		450		455	
170	ccc caa aaa cag tgt cga gaa gag gtg ctc aag aac ttc aca gac cag							1626
171	Pro Gln Lys Gln Cys Arg Glu Glu Val Leu Lys Asn Phe Thr Asp Gln							
172		460		465		470		
174	ctg cgg aag att tcc aag gat gcg ggg atg cct atc cag ggt caa cct							1674
175	Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly Gln Pro							
176		475		480		485		
178	tgt ttc tgc aaa tat gca cag ggg gca gac agc gtg gag cct atg ttc							1722
179	Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro Met Phe							
180		490		495		500		
182	cgg cat ctc aag aac acc tac tca ggg ctg cag ctc att att gtc atc							1770
183	Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile Val Ile							
184		505		510		515		
186	ctg cca ggg aag acg ccg gtg tat gct gag gtg aaa cgt gtc gga gat							1818
187	Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val Gly Asp							
188	520		525		530		535	
190	aca ctc ttg gga atg gct acg cag tgt gtg cag gtg aag aac gtg gtc							1866
191	Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn Val Val							
192		540		545		550		
194	aag acc tca cct cag act ctg tcc aac ctc tgc ctc aag atc aat gtc							1914
195	Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile Asn Val							
196		555		560		565		
198	aaa ctt ggt ggc att aac aac atc cta gtc cca cac cag cgc tct gcc							1962
199	Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg Ser Ala							
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204		585					590					595					
206	cca	gca	ggg	gat	ggg	aaa	aaa	cct	tct	atc	aca	gca	gtg	gta	ggc	agt	2058
207	Pro	Ala	Gly	Asp	Gly	Lys	Lys	Pro	Ser	Ile	Thr	Ala	Val	Val	Gly	Ser	
208	600					605					610					615	
210	atg	gat	gcc	cac	ccc	agc	cga	tac	tgt	gct	act	gtg	cgg	gta	cag	cga	2106
211	Met	Asp	Ala	His	Pro	Ser	Arg	Tyr	Cys	Ala	Thr	Val	Arg	Val	Gln	Arg	
212					620						625					630	
214	cca	cgg	caa	gag	atc	att	gaa	gac	ttg	tcc	tac	atg	gtg	cgt	gag	ctc	2154
215	Pro	Arg	Gln	Glu	Ile	Ile	Glu	Asp	Leu	Ser	Tyr	Met	Val	Arg	Glu	Leu	
216					635					640						645	
218	ctc	atc	caa	ttc	tac	aag	tcc	acc	cgt	ttc	aag	cct	acc	cgc	atc	atc	2202
219	Leu	Ile	Gln	Phe	Tyr	Lys	Ser	Thr	Arg	Phe	Lys	Pro	Thr	Arg	Ile	Ile	
220					650						655					660	
222	ttc	tac	cga	gat	ggg	gtg	cct	gaa	ggc	cag	cta	ccc	cag	ata	ctc	cat	2250
223	Phe	Tyr	Arg	Asp	Gly	Val	Pro	Glu	Gly	Gln	Leu	Pro	Gln	Ile	Leu	His	
224							670					675					
226	tat	gag	cta	ctg	gcc	att	cgt	gat	gcc	tgc	atc	aaa	ctg	gaa	aag	gac	2298
227	Tyr	Glu	Leu	Leu	Ala	Ile	Arg	Asp	Ala	Cys	Ile	Lys	Leu	Glu	Lys	Asp	
228	680						685					690				695	
230	tac	cag	cct	ggg	atc	act	tat	att	gtg	gtg	cag	aaa	cgc	cat	cac	acc	2346
231	Tyr	Gln	Pro	Gly	Ile	Thr	Tyr	Ile	Val	Val	Gln	Lys	Arg	His	His	Thr	
232						700						705				710	
234	cgc	ctt	ttc	tgt	gct	gac	aag	aat	gag	cga	att	ggg	aag	agt	ggt	aac	2394
235	Arg	Leu	Phe	Cys	Ala	Asp	Lys	Asn	Glu	Arg	Ile	Gly	Lys	Ser	Gly	Asn	
236							715					720				725	
238	atc	cca	gct	ggg	acc	aca	gtg	gac	acc	aac	atc	acc	cac	cca	ttt	gag	2442
239	Ile	Pro	Ala	Gly	Thr	Thr	Val	Asp	Thr	Asn	Ile	Thr	His	Pro	Phe	Glu	
240							730					735				740	
242	ttt	gac	ttc	tat	ctg	tgc	agc	cac	gca	ggc	atc	cag	ggc	acc	agc	cga	2490
243	Phe	Asp	Phe	Tyr	Leu	Cys	Ser	His	Ala	Gly	Ile	Gln	Gly	Thr	Ser	Arg	
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246	cca	tcc	cat	tac	tat	gtt	ctt	tgg	gat	gac	aac	cgt	ttc	aca	gca	gat	2538
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248	760						765					770				775	
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252							780					785				790	
254	aca	cgc	tct	gtc	tct	atc	cca	gca	cct	gcc	tac	tat	gcc	cgc	ctg	gtg	2634
255	Thr	Arg	Ser	Val	Ser	Ile	Pro	Ala	Pro	Ala	Tyr	Tyr	Ala	Arg	Leu	Val	
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258	gct	ttc	cgg	gca	cga	tac	cac	ctg	gtg	gac	aag	gag	cat	gac	agt	gga	2682
259	Ala	Phe	Arg	Ala	Arg	Tyr	His	Leu	Val	Asp	Lys	Glu	His	Asp	Ser	Gly	
260							810					815				820	
262	gag	ggg	agc	cac	ata	tcg	ggg	cag	agc	aat	ggg	cgg	gac	ccc	cag	gcc	2730
263	Glu	Gly	Ser	His	Ile	Ser	Gly	Gln	Ser	Asn	Gly	Arg	Asp	Pro	Gln	Ala	
264							825					830				835	
266	ctg	gcc	aaa	gcc	gtg	cag	gtt	cac	cag	gat	act	ctg	cgc	acc	atg	tac	2778

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Output Set: N:\CRF3\12312001\J007078.raw

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267 Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met Tyr
268 840                      845                      850                      855
270 ttc gct tga aggcagaacg ctgttacctc actggataga agaaagcttt ccaagcccca 2837
271 Phe Ala
274 ggagctgtgc cacccaaate cagaggaagc aaggaggagg gaggtggggg agggaggagt 2897
275 gtaggatgcc ttgtttcctt ctatagaggt ggtgtaagag tggggaacag ggccagcaag 2957
276 acagaccacc agccagaaat ctctgatata aacctcatgt ccccccaccc tcaccccata 3017
277 ttgtcacata tggccctgac cccactggac caaaaggggc agcaactggtg cccaccatac 3077
278 acacaggtgt ctcatgtgac tcacagtgtt aaagactcat gcttgacagc ttggttaagg 3137
279 caactctgta gccctgcaga caaaagctgg ttaggttttg gtttgatact ttagatggga 3197
280 aagtgagggg cttgagaaaag tgggtgggag gagggaagga ttttttagga gccttaatac 3257
281 gaaaaggact agatttggtt aagaagaaaa atgaaaccag acccagatca atattttagg 3317
282 atactagatg ttttaattggg ttcagaatcc agtttgtagg aagatttttt atgggttttg 3377
283 gttgtctctc cccagctgc cccccccac cttaccctta ttctctctg tccacatttt 3437
284 ctgccccacc ttaattctcc tccctgacag acatccagcc cctagtaata ctttaaggca 3497
285 tatggcaact agctttgaag tgacacgacc ctgtcttctc tccgcccgtt ggtgggtaac 3557
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317 taaaaagcaa gagaatcagc tttgggcaat gacaagaaat gagttcttac tctgattttt 5477
318 ttgtaaaaag ataatttttg agacttgaaa aataccccga ccttgagatt attcctgttt 5537

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 12/31/2001

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10